

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Diacylglycerol Acyltransferases

<130> BB1295

<140>

<141>

<150> 60/110,602

<151> 1998-12-02

<150> 60/127,111

<151> 1999-03-31

<160> 26

<170> Microsoft Office 97

<210> 1

<211> 1888

<212> DNA

<213> Arabidopsis thaliana

<400> 1

```

gcttcttctt tcaatccgct ctttccctct ccattagatt ctgtttctct tttcaatttc 60
ttctgcatgc ttctcgatgc tctctgacgc ctcttttctc ccgacgctgt ttctgcaaac 120
gcttttcgaa atggcgattt tggattctgc tggcgttact acggtgacgg agaacggtgg 180
cggagagttc gtcgatcttg ataggcttcg tcgacggaaa tcgagatcgg attcttctaa 240
cggacttctt ctctctgggt ccgataataa ttctccttcg gatgatgttg gagctcccg 300
cgacgttagg gatcggattg attccggtgt taacgatgac gctcagggaa cagccaattt 360
ggccggagat aataacggtg gtggcgataa taacggtggt ggaagaggcg gcggagaagg 420
aagaggaaac gccgatgcta cgtttacgta tcgaccgtcg gttccagctc atcggagggc 480
gagagagagt ccacttagct ccgacgcaat cttcaaacag agccatgccg gattattcaa 540
cctctgtgta gtagttctta ttgctgtaaa cagtagactc atcatcgaaa atcttatgaa 600
gtatggttgg ttgatcagaa cggatttctg gtttagttca agatcgctgc gagattggcc 660
gcttttcatg tgttggatat ccctttcgat ctttctttg gctgccttta cggttgagaa 720
attggtactt cagaaatata tatcagaacc tgttggcatc ttcttctata ttattatcac 780
catgacagag gttttgtatc cagtttacgt caccctaagg tgtgattctg cttttttatc 840
agggttcact ttgatgctcc tcacttgcat tgtgtggcta aagttgggtt cttatgctca 900
tactagctat gacataagat ccctagccaa tgcagctgat aaggccaatc ctgaagtctc 960
ctactacgtt agcttgaaga gcttggcata tttcatggtc gctcccatat tgtgttatca 1020
gccaagttaa ccacgttctg catgtatacg gaagggttgg gtggctcgtc aatttgcaaa 1080
actggtcata ttcaccggat tcatgggatt tataatagaa caatatataa atcctattgt 1140
caggaactca aagcatcctt tgaaaggcga tcttctatat gctattgaaa gagtgttgaa 1200
gctttcagtt ccaaatttat atgtgtggtc ctgcatgttc tactgcttct tccacctttg 1260
gttaaacata ttggcagagc ttctctgctt cggggatcgt gaattctaca aagattggtg 1320
gaatgcaaaa agtgtgggag attactggag aatgtggaat atgcctgttc ataaatggat 1380
ggttcgacat atatacttcc cgtgcttgcg cagcaagata ccaaagacac tcgccartat 1440
cattgctttc ctagtctctg cagtctttca tgagctatgc atcgcagttc cttgtcgtct 1500
cttcaagcta tgggcttttc ttgggattat gtttcagggt cctttgggtc tcatcacaaa 1560
ctatctacag gaaaggtttg gctcaacggt ggggaacatg atcttctggt tcatcttctg 1620
cattttcgga caaccgatgt gtgtgcttct ttattaccac gacctgatga accgaaaagg 1680
atcgatgtca tgaaacaact gttcaaaaaa tgactttctt caaacatcta tggcctcggt 1740
ggatctccgt tgatgttgtg gtggttctga tgctaaaacg acaaatagtg ttataaccat 1800
tgaagaagaa aagaaaatta gattgttgt atctgcaaaa attttggtg agacacgcaa 1860
accggtttgg attttgttat ggagtaaa 1888

```

<210> 2
 <211> 520
 <212> PRT
 <213> Arabidopsis thaliana

<400> 2
 Met Ala Ile Leu Asp Ser Ala Gly Val Thr Thr Val Thr Glu Asn Gly
 1 5 10 15
 Gly Gly Glu Phe Val Asp Leu Asp Arg Leu Arg Arg Arg Lys Ser Arg
 20 25 30
 Ser Asp Ser Ser Asn Gly Leu Leu Leu Ser Gly Ser Asp Asn Asn Ser
 35 40 45
 Pro Ser Asp Asp Val Gly Ala Pro Ala Asp Val Arg Asp Arg Ile Asp
 50 55 60
 Ser Val Val Asn Asp Asp Ala Gln Gly Thr Ala Asn Leu Ala Gly Asp
 65 70 75 80
 Asn Asn Gly Gly Gly Asp Asn Asn Gly Gly Gly Arg Gly Gly Gly Glu
 85 90 95
 Gly Arg Gly Asn Ala Asp Ala Thr Phe Thr Tyr Arg Pro Ser Val Pro
 100 105 110
 Ala His Arg Arg Ala Arg Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe
 115 120 125
 Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Val Val Val Leu Ile
 130 135 140
 Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Trp
 145 150 155 160
 Leu Ile Arg Thr Asp Phe Trp Phe Ser Ser Arg Ser Leu Arg Asp Trp
 165 170 175
 Pro Leu Phe Met Cys Trp Ile Ser Leu Ser Ile Phe Pro Leu Ala Ala
 180 185 190
 Phe Thr Val Glu Lys Leu Val Leu Gln Lys Tyr Ile Ser Glu Pro Val
 195 200 205
 Gly Ile Phe Leu His Ile Ile Ile Thr Met Thr Glu Val Leu Tyr Pro
 210 215 220
 Val Tyr Val Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Val Thr
 225 230 235 240
 Leu Met Leu Leu Thr Cys Ile Val Trp Leu Lys Leu Val Ser Tyr Ala
 245 250 255
 His Thr Ser Tyr Asp Ile Arg Ser Leu Ala Asn Ala Ala Asp Lys Ala
 260 265 270
 Asn Pro Glu Val Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe
 275 280 285

WO 00/32756

Met Val Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Ser Ala
 290 295 300
 Cys Ile Arg Lys Gly Trp Val Ala Arg Gln Phe Ala Lys Leu Val Ile
 305 310 315 320
 Phe Thr Gly Phe Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile
 325 330 335
 Val Arg Asn Ser Lys His Pro Leu Lys Gly Asp Leu Leu Tyr Ala Ile
 340 345 350
 Glu Arg Val Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys
 355 360 365
 Met Phe Tyr Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu
 370 375 380
 Leu Cys Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys
 385 390 395 400
 Ser Val Gly Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp
 405 410 415
 Met Val Arg His Ile Tyr Phe Pro Cys Leu Arg Ser Lys Ile Pro Lys
 420 425 430
 Thr Leu Ala Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu
 435 440 445
 Leu Cys Ile Ala Val Pro Cys Arg Leu Phe Lys Leu Trp Ala Phe Leu
 450 455 460
 Gly Ile Met Phe Gln Val Pro Leu Val Phe Ile Thr Asn Tyr Leu Gln
 465 470 475 480
 Glu Arg Phe Gly Ser Thr Val Gly Asn Met Ile Phe Trp Phe Ile Phe
 485 490 495
 Cys Ile Phe Gly Gln Pro Met Cys Val Leu Leu Tyr Tyr His Asp Leu
 500 505 510
 Met Asn Arg Lys Gly Ser Met Ser
 515 520

<210> 3
 <211> 1281
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (356)

<220>
 <221> unsure
 <222> (427)

<220>
 <221> unsure
 <222> (1188)

<220>
 <221> unsure
 <222> (1196)

<220>
 <221> unsure
 <222> (1198)

<220>
 <221> unsure
 <222> (1236)

<220>
 <221> unsure
 <222> (1242)

<220>
 <221> unsure
 <222> (1244)

<220>
 <221> unsure
 <222> (1248)

<220>
 <221> unsure
 <222> (1259)

<220>
 <221> unsure
 <222> (1266)

<220>
 <221> unsure
 <222> (1280)

<400> 3
 tttaaatgcta catcattgcg agactggcca ctgctaattgt gttgccttag tctacccata 60
 tttccccttg gtgcatttgc agtcgaaaag ttggcattca acaatctcgt tagtgatcct 120
 gctactacct gttttcacat cttttttaca acatttgaaa ttgtatatcc agtgctcgtg 180
 attcttaagt gtgattctgc agttttatca ggctttgtgt tgatgtttat tgccctgcatt 240
 gtttggtgta agcttgtatc ttttgcacat acaaaccatg atataaggaa aactgatcac 300
 aagcggcaag aaggttgata atgaactgac cgcggctggc atagataatt tacaanctcc 360
 aactcttggg agtctaacat acttcaagat ggctccgaca ctctgttatc aagccaaagt 420
 tatectncga acaccttatg ttagaaaagg ttggctgggc cgtcaagtta ttctatactt 480
 gatatttact ggtctccaag gattcattat tgagcaatac ataaatccta ttgttgtgaa 540
 ctctcaacat ccattgatgg gaggattact gaatgctgta gagactgttt tgaagctctc 600
 attaccaaatt gtctacctgt ggctttgcat gttttattgc cttttccatc tgtgggttaa 660
 catacttgct gagattcttc gatttggtga ccgagaattc tacaaagact ggtggaatgc 720
 aaagacaatt gatgagtact ggagaaaatg gaacatgcct gtgcataaat ggattgttcg 780
 tcatatatat ttcccttgca tgcgaaatgg tatatcaaag gaagttgctg tttttatata 840
 gttctttgtt tctgctgtac ttcattgagt atgtgttgct gttccctgcc acataactcaa 900
 gttctgggct ttcttaggaa tcatgcttca gattcccctc atcatattga catcatacct 960
 caaaaataaa ttcagtgcga caatggttgg caatatgac ttttggtttt ttttctgcat 1020
 atacgggcag ccaatgtgtg ttctattgta ttaccatgat gtgatgaacc ggactgagaa 1080
 ggcaaaaataa ccattctgtg atcttttttg gtttcatttc tccatcatgg aaactgaaac 1140

ataactgtgc acacataaac agcatcgtgt ctcaattttt taaaaaanaa aagaananca 1200
 caaaaaaccc agggggggccg gtaccaatcc ccaaantatc gntnaccncc cagggcgtnt 1260
 taaacncgta cggaaaaccn g 1281

<210> 4
 <211> 361
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (119)

<400> 4
 Phe Asn Ala Thr Ser Leu Arg Asp Trp Pro Leu Leu Met Cys Cys Leu
 1 5 10 15
 Ser Leu Pro Ile Phe Pro Leu Gly Ala Phe Ala Val Glu Lys Leu Ala
 20 25 30
 Phe Asn Asn Leu Val Ser Asp Pro Ala Thr Thr Cys Phe His Ile Leu
 35 40 45
 Phe Thr Thr Phe Glu Ile Val Tyr Pro Val Leu Val Ile Leu Lys Cys
 50 55 60
 Asp Ser Ala Val Leu Ser Gly Phe Val Leu Met Phe Ile Ala Cys Ile
 65 70 75 80
 Val Trp Leu Lys Leu Val Ser Phe Ala His Thr Asn His Asp Ile Gly
 85 90 95
 Lys Leu Ile Thr Ser Gly Lys Lys Val Asp Asn Glu Leu Thr Ala Ala
 100 105 110
 Gly Ile Asp Asn Leu Gln Xaa Pro Thr Leu Gly Ser Leu Thr Tyr Phe
 115 120 125
 Lys Met Ala Pro Thr Leu Cys Tyr Gln Ala Lys Val Ile Leu Arg Thr
 130 135 140
 Pro Tyr Val Arg Lys Gly Trp Leu Val Arg Gln Val Ile Leu Tyr Leu
 145 150 155 160
 Ile Phe Thr Gly Leu Gln Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro
 165 170 175
 Ile Val Val Asn Ser Gln His Pro Leu Met Gly Gly Leu Leu Asn Ala
 180 185 190
 Val Glu Thr Val Leu Lys Leu Ser Leu Pro Asn Val Tyr Leu Trp Leu
 195 200 205
 Cys Met Phe Tyr Cys Leu Phe His Leu Trp Leu Asn Ile Leu Ala Glu
 210 215 220
 Ile Leu Arg Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala
 225 230 235 240

Lys Thr Ile Asp Glu Tyr Trp Arg Lys Trp Asn Met Pro Val His Lys
 245 250 255
 Trp Ile Val Arg His Ile Tyr Phe Pro Cys Met Arg Asn Gly Ile Ser
 260 265 270
 Lys Glu Val Ala Val Phe Ile Ser Phe Phe Val Ser Ala Val Leu His
 275 280 285
 Glu Tyr Val Leu Leu Phe Leu His Ile Leu Lys Phe Trp Ala Phe Leu
 290 295 300
 Gly Ile Met Leu Gln Ile Pro Leu Ile Ile Leu Thr Ser Tyr Leu Lys
 305 310 315 320
 Asn Lys Phe Ser Asp Thr Met Val Gly Asn Met Ile Phe Trp Phe Phe
 325 330 335
 Phe Cys Ile Tyr Gly Gln Pro Met Cys Val Leu Leu Tyr Tyr His Asp
 340 345 350
 Val Met Asn Arg Thr Glu Lys Ala Lys
 355 360

<210> 5
 <211> 978
 <212> DNA
 <213> Zea mays

<400> 5
 ggcacgaggt tagaaaaggt tggctggtcc gtcaagttat tctatacttg atatttactg 60
 gtcctcaagg attcattatt gagcaataca taaatcctat tgttggtgaac tctcaacatc 120
 cattgatggg aggattactg aatgctgtag agactgtttt gaagctctca ttaccaaagt 180
 tctacctgtg gctttgcatg ttttattgcc ttttccatct gtgggttaaac atacttgctg 240
 agattcttcg atttggtgac cgagaattct acaaagactg gtggaatgca aagacaattg 300
 atgagtactg gagaaaatgg aacatgcctg tgcataaatg gattgttcgt catatatatt 360
 tcccttgcat gcgaaatggt atatcaaagg aagttgctgt ttttatatcg ttctttgttt 420
 ctgctgtact tcatgagctg cagattactt ggatgaagtg ctctatataa aattaaatat 480
 ttcataatcc agtcccttcc gagaaaatta tgatacattt tgtttgcaat tgtacaccag 540
 ttatgtgttg ctgttccctg ccacatactc aagttctggg ctttcttagg aatcatgctt 600
 cagattcccc tcatcatatt gacatcatac ctcaaaaata aattcagtga cacaatgcc 660
 atgtgtgttc tattgtatta ccatgatgtg atgaaccgga ctgagaaggc aaaataacca 720
 tctgtagatc ttttttggtg tttcatttct tccatcatgg aaactgaaag caataatctg 780
 tgcacacagt aaaccagcat cgtgtcttcc agtttttttt gttgttggtg gaatctatcc 840
 tagatcttta tcatgtgtat ggtggataac ctcatgtcac catcgatatc gtataacaata 900
 agcctaaatc agctgacgtt ctatatgtaa attagtaaat gtaatgacta attagtgcc 960
 aaaaaaaaaa aaaaaaaaaa 978

<210> 6
 <211> 155
 <212> PRT
 <213> Zea mays

<400> 6
 His Glu Val Arg Lys Gly Trp Leu Val Arg Gln Val Ile Leu Tyr Leu
 1 5 10 15
 Ile Phe Thr Gly Leu Gln Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro
 20 25 30

Ile Val Val Asn Ser Gln His Pro Leu Met Gly Gly Leu Leu Asn Ala
 35 40 45
 Val Glu Thr Val Leu Lys Leu Ser Leu Pro Asn Val Tyr Leu Trp Leu
 50 55 60
 Cys Met Phe Tyr Cys Leu Phe His Leu Trp Leu Asn Ile Leu Ala Glu
 65 70 75 80
 Ile Leu Arg Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala
 85 90 95
 Lys Thr Ile Asp Glu Tyr Trp Arg Lys Trp Asn Met Pro Val His Lys
 100 105 110
 Trp Ile Val Arg His Ile Tyr Phe Pro Cys Met Arg Asn Gly Ile Ser
 115 120 125
 Lys Glu Val Ala Val Phe Ile Ser Phe Phe Val Ser Ala Val Leu His
 130 135 140
 Glu Leu Gln Ile Thr Trp Met Lys Cys Ser Ile
 145 150 155

<210> 7
 <211> 1559
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (1542)..(1543)

<220>
 <221> unsure
 <222> (1555)..(1556)

<400> 7
 ttttggttta atgctacatc attgcgagac tggccactgc taatgtgttg ccttagtcta 60
 cccatatttc cccttggtgc atttgcagtc gaaaagttag cattcaacaa tctcgtagt 120
 gatcctgcta ctacctgttt tcacatcctt ttacaacat ttgaaattgt atatccagt 180
 ctcgtagtgc ttaagtgtga ttctgcagtt ttatcaggct ttgtgttgat gtttattgcc 240
 tgcattgttt ggctgaagct tgtatctttt gcacatacaa accatgatat aagaaaactg 300
 atcacaagcg gcaagaaggt tgataatgaa ctgaccgcgg ctggcataga taatttacia 360
 gctccaactc ttgggagttc aacatacttc atgatggctc cgacactctg ttatcagcca 420
 agttatcctc gaacacctta tgtagaaaaa ggttggctgg tccgtcaagt tattctatac 480
 ttgatattta ctgggtctcca aggattcatt attgagcaat acataaatcc tattgttgtg 540
 aactctcaac atccattgat gggaggatta ctgaatgctg tagagactgt tttgaagctc 600
 tcattaccaa atgtctacct gtggctttgc atgttttatt gccttttcca tctgtggta 660
 aacatacttg ctgagattct tcgatttggg gaccgagaat tctacaaaga ctggtggaat 720
 gcaaagacaa ttgatgagta ctggagaaaa tggaaactgc ctgtgcataa atggattgtt 780
 cgtcatatat attttccttg catgcgaaat ggtatatcaa aggaagttag tgtttttata 840
 tegtctcttg tttctgctgt acttcatgag gtaacttatt tactttttca ctcttcatct 900
 gcatatatta attatatagt tctctatttt caaatgtgtc ctttcgagtt tcgacatgct 960
 tttgttcaaa cttaccagct gtagattact tggatgaagt gctctatata aaattcaata 1020
 tttcacaate cagtcctttt cgagaaaaatt atgatacatt ttgtttgcat ttgtacacca 1080
 gttatgcgtt gcagttccct gccacatact caagtctctg gctttcttag gaatcatgct 1140
 tcgattccc ctcatcatat tgacatcata cctcaaaaat aaattcagtg acacaatggt 1200
 tggcaatatg atcttttggg tttttttctg catatacggg cagccaatgt gtgttctatt 1260
 gtattaccat gatgtgatga accggactga gaaggcaaaa taaccatctg tagatctttt 1320

ttggtgtttc atttctgcca tcatggaaac tgaaagcaat aatctgtgca cacagtaaac 1380
 cagcatcgtg tcttccagtt ttctttttgt tgttggaatc tctcctagat ctttatcatg 1440
 tgtatggtgg ataacctcat gtcaccatcg tatctgtata caataagcct aaatcagctg 1500
 acgttatata tgtataatta gtaaagttag cgataaatgt cnnccccctg agagnnacg 1559

<210> 8
 <211> 327
 <212> PRT
 <213> Zea mays

<400> 8
 Phe Trp Phe Asn Ala Thr Ser Leu Arg Asp Trp Pro Leu Leu Met Cys
 1 5 10 15
 Cys Leu Ser Leu Pro Ile Phe Pro Leu Gly Ala Phe Ala Val Glu Lys
 20 25 30
 Leu Ala Phe Asn Asn Leu Val Ser Asp Pro Ala Thr Thr Cys Phe His
 35 40 45
 Ile Leu Phe Thr Thr Phe Glu Ile Val Tyr Pro Val Leu Val Ile Leu
 50 55 60
 Lys Cys Asp Ser Ala Val Leu Ser Gly Phe Val Leu Met Phe Ile Ala
 65 70 75 80
 Cys Ile Val Trp Leu Lys Leu Val Ser Phe Ala His Thr Asn His Asp
 85 90 95
 Ile Arg Lys Leu Ile Thr Ser Gly Lys Lys Val Asp Asn Glu Leu Thr
 100 105 110
 Ala Ala Gly Ile Asp Asn Leu Gln Ala Pro Thr Leu Gly Ser Leu Thr
 115 120 125
 Tyr Phe Met Met Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg
 130 135 140
 Thr Pro Tyr Val Arg Lys Gly Trp Leu Val Arg Gln Val Ile Leu Tyr
 145 150 155 160
 Leu Ile Phe Thr Gly Leu Gln Gly Phe Ile Ile Glu Gln Tyr Ile Asn
 165 170 175
 Pro Ile Val Val Asn Ser Gln His Pro Leu Met Gly Gly Leu Leu Asn
 180 185 190
 Ala Val Glu Thr Val Leu Lys Leu Ser Leu Pro Asn Val Tyr Leu Trp
 195 200 205
 Leu Cys Met Phe Tyr Cys Leu Phe His Leu Trp Leu Asn Ile Leu Ala
 210 215 220
 Glu Ile Leu Arg Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn
 225 230 235 240
 Ala Lys Thr Ile Asp Glu Tyr Trp Arg Lys Trp Asn Met Pro Val His
 245 250 255

Lys Trp Ile Val Arg His Ile Tyr Phe Pro Cys Met Arg Asn Gly Ile
 260 265 270
 Ser Lys Glu Val Ala Val Phe Ile Ser Phe Phe Val Ser Ala Val Leu
 275 280 285
 His Glu Val Thr Tyr Leu Leu Phe His Ser Ser Ser Ala Tyr Ile Asn
 290 295 300
 Tyr Ile Val Leu Tyr Phe Gln Met Cys Pro Phe Glu Phe Arg His Ala
 305 310 315 320
 Phe Val Gln Thr Tyr Gln Leu
 325

<210> 9
 <211> 901
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (491)

<220>
 <221> unsure
 <222> (577)

<220>
 <221> unsure
 <222> (806)

<220>
 <221> unsure
 <222> (893)

<400> 9
 ccggaattcc cgggtcgacc cagcggtccg gtctcttatg cacatacaaa ttatgatata 60
 agggatattgt ccaaaagtac tgagaagggt gctgcatatg gaaattatgt cgatcctgag 120
 aatatgaaag atccaacctt taaaagtcta gtgtacttca tgttggtccc aacactttgt 180
 taccagccaa cttatcctca aactacatgt attagaaagg gttgggtgac ccagcaactc 240
 ataaagtgcg tggtttttac aggcctgatg ggcttcataa ttgagcaata tataaaccca 300
 attgtgaaga attccaaaca tccactgaaa gggaattttt tgaatgctat agaaagagtc 360
 ttaaaactct cagtgccaac attatatgta tggctttgca tgttctattg cttttttcat 420
 ttatggctga acattgtagc ttaactcctc tgtttcggtg accgtgaatt ctataaggac 480
 tgggtggaatg ncaaaactgt tgaagagtac tggaggatgt ggaacatgcc tgttcataag 540
 tggatcatca gacacatata ttttccatgt ataaggnaag gcttttccag ggggtgtagct 600
 attctaattct cgtttctggt ttcagctgta ttccatgaga tatgtattgc ggtgcccgtgc 660
 cacattttca aattctgggc attttctggg atcatgtttc agataccgtt ggtattcttg 720
 acaagatata tccatgctac gttcaagcat gtaatgggtg gcaacatgat attttggttc 780
 ttcagtatag tccgacagcc gatgtngtgt ctctataact aacatgacgt catgaaacaa 840
 gcaaggccaa gcaagtagat agttcggcag agacatgtaa cttcaacatc gancatcaga 900
 a 901

<210> 10
 <211> 285
 <212> PRT
 <213> Zea mays

<220>

<221> UNSURE

<222> (148)

<220>

<221> UNSURE

<222> (164)

<220>

<221> UNSURE

<222> (193)

<220>

<221> UNSURE

<222> (269)

<220>

<221> UNSURE

<222> (274)

<400> 10

Pro Glu Phe Pro Gly Arg Pro Thr Arg Pro Val Ser Tyr Ala His Thr
 1 5 10 15

Asn Tyr Asp Ile Arg Val Leu Ser Lys Ser Thr Glu Lys Gly Ala Ala
 20 25 30

Tyr Gly Asn Tyr Val Asp Pro Glu Asn Met Lys Asp Pro Thr Phe Lys
 35 40 45

Ser Leu Val Tyr Phe Met Leu Ala Pro Thr Leu Cys Tyr Gln Pro Thr
 50 55 60

Tyr Pro Gln Thr Thr Cys Ile Arg Lys Gly Trp Val Thr Gln Gln Leu
 65 70 75 80

Ile Lys Cys Val Val Phe Thr Gly Leu Met Gly Phe Ile Ile Glu Gln
 85 90 95

Tyr Ile Asn Pro Ile Val Lys Asn Ser Lys His Pro Leu Lys Gly Asn
 100 105 110

Phe Leu Asn Ala Ile Glu Arg Val Leu Lys Leu Ser Val Pro Thr Leu
 115 120 125

Tyr Val Trp Leu Cys Met Phe Tyr Cys Phe Phe His Leu Trp Leu Asn
 130 135 140

Ile Val Ala Xaa Leu Leu Cys Phe Gly Asp Arg Glu Phe Tyr Lys Asp
 145 150 155 160

Trp Trp Asn Xaa Lys Thr Val Glu Glu Tyr Trp Arg Met Trp Asn Met
 165 170 175

Pro Val His Lys Trp Ile Ile Arg His Ile Tyr Phe Pro Cys Ile Arg
 180 185 190

Xaa Gly Phe Ser Arg Gly Val Ala Ile Leu Ile Ser Phe Leu Val Ser
 195 200 205

Ala Val Phe His Glu Ile Cys Ile Ala Val Pro Cys His Ile Phe Lys
 210 215 220

Phe Trp Ala Phe Ser Gly Ile Met Phe Gln Ile Pro Leu Val Phe Leu
 225 230 235 240

Thr Arg Tyr Leu His Ala Thr Phe Lys His Val Met Val Gly Asn Met
 245 250 255

Ile Phe Trp Phe Phe Ser Ile Val Arg Gln Pro Met Xaa Cys Leu Tyr
 260 265 270

Asn Xaa His Asp Val Met Lys Gln Ala Arg Pro Ser Lys
 275 280 285

<210> 11
 <211> 254
 <212> DNA
 <213> Oryza sativa

<400> 11
 ggcatacggc ggtggggact tctccgcgtt cacgttccgc gcggcggcgc cggcgcaccg 60
 caaggccaag gagagcccc tcagctccga cgccatcttc aagcagagtc atgcaggcct 120
 tttcaacctt tgcattgttg ttctagttgc agtgaacagc aggcttatta tcgagaactt 180
 aatgaagtat ggcttattaa taagagctgg gttttggttt aatgataaat cattgcggga 240
 ctggccactt ctaa 254

<210> 12
 <211> 80
 <212> PRT
 <213> Oryza sativa

<400> 12
 Ala Tyr Gly Gly Gly Asp Phe Ser Ala Phe Thr Phe Arg Ala Ala Ala
 1 5 10 15

Pro Val His Arg Lys Ala Lys Glu Ser Pro Leu Ser Ser Asp Ala Ile
 20 25 30

Phe Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Ile Val Val Leu
 35 40 45

Val Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly
 50 55 60

Leu Leu Ile Arg Ala Gly Phe Trp Phe Asn Asp Lys Ser Leu Arg Asp
 65 70 75 80

<210> 13
 <211> 1587
 <212> DNA
 <213> Oryza sativa

<400> 13
 gcacgagggc atacggcggg ggggacttct ccgcgttcac gttccgcgcg gcggcgcggc 60
 tgcaccgcaa ggccaaggag agccccctca gctccgacgc catcttcaag cagagtcattg 120
 caggcctttt caacctatgc attgttggtc tagttgcagt gaacagcagg ctattattcg 180
 agaacttaat gaagtatggc ttattaataa gagctgggtt ttggtttaat gataaatcat 240
 tgcgggactg gccacttcta atgtgttgct ttagtctgcc tgctttcccc ctgggtgcat 300
 ttgcagttga aaagttggca ttaacaatg ttattactga tgctgttgct acctgcctcc 360

```

atatcttcct ttcaacaacc gaaattgtat atccagtgtc tgtgattctt aagtgtgatt 420
ctgcagtttt gtctggcttt ttgttgatat ttattgcctg tattgtttgg ctgaagcttg 480
tatcttttgc acatacaaac catgatataa ggcaactgac catgggcggc aagaaggttg 540
ataatgaact aagcacagtt gacatggata atttacaacc tccaacttta gggaatctaa 600
tatacttcat gatggctcct acactctgtt atcagccaag ctatccccga acttcatgtg 660
ttagaaaagg ttggtgatt cgtcaaatta ttctgtactt gatctttact ggtcttcaag 720
gcttcattat tgagcaatac ataaatccaa ttgttgtaa ttctcagcat ccattgaaag 780
gaggactcct aaatgctgta gagactgttt tgaaactctc attaccaaatt gtttacctgt 840
ggctttgcat gttctatgct tttttccatc tctggttaag tatacttgct gagattcttc 900
gatttggtga ccgtgaattc tacaaagatt ggtggaatgc aaaaacaatt gatgagtatt 960
ggagaaaatg gaatatgcct gtacataaat ggggtgttcg ccatatttac tttccttgca 1020
tgcgaaatgg tatatcaaag gaagttgctg tcttgatata attccttggt tctgccgtac 1080
tccatgagat atgtgtcgt gttccctgcc gcatttctcaa gttctgggca ttttaggaa 1140
taatgctaca gatccccctt atcgtattga cagcatacct caaaagtaaa ttcagagata 1200
caatggttgg caacatgata ttttggttct ttttctgcat ctatgggcag ccaatgtgcc 1260
ttctcctgta ctatcatgat gtgatgaaca ggattgagaa ggcaagataa atgcgtgttg 1320
ccatcttttt cctctgtttc attttgtagc agcagaagca caagcaataa tccacatgct 1380
agccataaaa cagcatgatt cccaacggtg tggtagagcc aaccttcctg ttattctatt 1440
ttcttggtg tgggtgtagat ttagttttta acttggtggt aaccgcagga atgcctgtag 1500
ataagcatct gtcattctgt ctggcgacgt tctccttatt aatgtgtaga tgtagaactg 1560
tttccgaaaa aaaaaaaaaa aaaaaaa 1587

```

<210> 14
 <211> 500
 <212> PRT
 <213> *Oryza sativa*

<400> 14
 Met Val Gly Ser Asp Gly Asp Gly Gly Gly Gly Glu Ala His
 1 5 10 15
 Ala Gly Gly Pro Arg Arg Arg Ala Gly Gln Leu Arg Gly Arg Leu Arg
 20 25 30
 Asp Glu Ala Ala Pro Gly Ser Pro Pro Arg Pro Arg Pro Arg Pro Arg
 35 40 45
 Pro Arg Gly Gly Asp Ser Asn Gly Arg Ser Val Leu Arg Pro Gly Gly
 50 55 60
 Gly Gly Gly Arg Gly Gly Gly Gly Asp Phe Ser Ala Phe Thr Phe Arg
 65 70 75 80
 Ala Ala Ala Pro Val His Arg Lys Ala Lys Glu Ser Pro Leu Ser Ser
 85 90 95
 Asp Ala Ile Phe Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Ile
 100 105 110
 Val Val Leu Val Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met
 115 120 125
 Lys Tyr Gly Leu Leu Ile Arg Ala Gly Phe Trp Phe Asn Asp Lys Ser
 130 135 140
 Leu Arg Asp Trp Pro Leu Leu Met Cys Cys Leu Ser Leu Pro Ala Phe
 145 150 155 160
 Pro Leu Gly Ala Phe Ala Val Glu Lys Leu Ala Phe Asn Asn Val Ile
 165 170 175

Thr Asp Ala Val Ala Thr Cys Leu His Ile Phe Leu Ser Thr Thr Glu
 180 185 190
 Ile Val Tyr Pro Val Leu Val Ile Leu Lys Cys Asp Ser Ala Val Leu
 195 200 205
 Ser Gly Phe Leu Leu Ile Phe Ile Ala Cys Ile Val Trp Leu Lys Leu
 210 215 220
 Val Ser Phe Ala His Thr Asn His Asp Ile Arg Gln Leu Thr Met Gly
 225 230 235 240
 Gly Lys Lys Val Asp Asn Glu Leu Ser Thr Val Asp Met Asp Asn Leu
 245 250 255
 Gln Pro Pro Thr Leu Gly Asn Leu Ile Tyr Phe Met Met Ala Pro Thr
 260 265 270
 Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Thr Ser Cys Val Arg Lys Gly
 275 280 285
 Trp Leu Ile Arg Gln Ile Ile Leu Tyr Leu Ile Phe Thr Gly Leu Gln
 290 295 300
 Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile Val Val Asn Ser Gln
 305 310 315 320
 His Pro Leu Lys Gly Gly Leu Leu Asn Ala Val Glu Thr Val Leu Lys
 325 330 335
 Leu Ser Leu Pro Asn Val Tyr Leu Trp Leu Cys Met Phe Tyr Ala Phe
 340 345 350
 Phe His Leu Trp Leu Ser Ile Leu Ala Glu Ile Leu Arg Phe Gly Asp
 355 360 365
 Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys Thr Ile Asp Glu Tyr
 370 375 380
 Trp Arg Lys Trp Asn Met Pro Val His Lys Trp Val Val Arg His Ile
 385 390 395 400
 Tyr Phe Pro Cys Met Arg Asn Gly Ile Ser Lys Glu Val Ala Val Leu
 405 410 415
 Ile Ser Phe Leu Val Ser Ala Val Leu His Glu Ile Cys Val Ala Val
 420 425 430
 Pro Cys Arg Ile Leu Lys Phe Trp Ala Phe Leu Gly Ile Met Leu Gln
 435 440 445
 Ile Pro Leu Ile Val Leu Thr Ala Tyr Leu Lys Ser Lys Phe Arg Asp
 450 455 460
 Thr Met Val Gly Asn Met Ile Phe Trp Phe Phe Phe Cys Ile Tyr Gly
 465 470 475 480
 Gln Pro Met Cys Leu Leu Leu Tyr Tyr His Asp Val Met Asn Arg Ile
 485 490 495

Glu Lys Ala Arg
500

<210> 15
<211> 1942
<212> DNA
<213> Glycine max

<400> 15
tagaaaacac gctcgggtctt ctctccaat ggcgatttcc gatgagcctg aaagtgtagc 60
cactgctctc aaccactctt cctgcgcgcg ccgtccctcc gccacctcca ccgccggcct 120
cttcaattcg cctgagacaa ccaccgacag ttccgggtgat gacttggcca aggattctgg 180
ttccgacgac tccatcaaca gcgacgacgc cgcctaccgt ccttccgtcc ccgctcaccg 240
acaagacact gatttctccg tccctcaaatt cgcctaccgt ccttccgtcc ccgctcaccg 300
caaagtgaag gaaagtccgc tcagctccga cactatttcc cgtcagagtc acgcgggcct 360
cttcaacctt tgtatagtag tccttggtgc tgtgaatagc cgactcatca ttgagaattt 420
aatgaagtat ggttggttga tcaaactctg cttttggttt agttcaaagt cattgagaga 480
ctggccctt ttcatgtgtt gtctttctct tgtggtatct cctttcgtct cctttatagt 540
ggagaagttg gcacaacgga agtggtatacc cgaaccagtt gttgtgtgtac ttcataataat 600
cattacctca acttcgcttt tctatccagt tttagttatt ctcaggtgtg attctgcttt 660
tgtatcaggt gtcacgttaa tgetgttttc ttgtgttgta tgggttaaaat tgggtgtctta 720
tgcacataca aactatgata tgagagcact taccaaatta gttgaaaagg gagaagcact 780
gctcgatact ctgaacatgg actatcccta caacgtaagc ttcaagagct tggcatattt 840
cctggttgcc cctacattat gttaccagcc aagctatcct cgcacacctt atattcgaaa 900
gggttggttg tttcgccaac ttgtcaagct gataatattt acaggagtta tgggatttat 960
aatagaccaa tatattaatc ccatagtaca aaattcacag catcctctca agggaaacct 1020
tctttacgcc accgagagag ttctgaagct ttctgttcca aatttatatg tgtggctctg 1080
catgttctat tgctttttcc acccttggtt aaatatcctg gcagagcttc ttcgatttgg 1140
tgatcgtgaa ttctacaagg attggtggaa tgccaaaact gtcgaagatt attggaggat 1200
gtggaatatg cctgttcaca aatggatgat ccgccacctt tattttccat gtttaaggca 1260
cgggtctacca aaggctgctg ctcttttaatt tgccttcctg gtttctgctt tattccatga 1320
gctgtgcatt gctgttcctt gccacatatt caagttgtgg gctttcgggt gaattatgtt 1380
tcaggttcct ttggtcttga tcaactaatta tctgcaaaat aaattcagaa actcaatggt 1440
tggaatatg attttttggg tcatattcag tatecttggg caacctatgt gtgtactgct 1500
atactaccat gacttgatga ataggaaagg caaacttgac tgaagctacg gccattacat 1560
tttaaagggtg cacatggatg agcttttcag ttttcagatt gtaaaattga tgtggatatg 1620
ttggtcaata tttgttttct acgaatgctt tcatctacca tggcattggc tgctctgaag 1680
gaattccacg ggatatgcca gttcacgagg ctaattcatt atcttgatct atgtacttac 1740
caactctcct ctggcaattg tatcaaaata tgcaattttg agagccatcc actggcattg 1800
ataactgcca aggaacactc taactgtttt ctgttaactg ttaattagta gagggctaga 1860
tgtaaatggt ttatgctcaa tatatttatt tcctcctaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aa 1942

<210> 16
<211> 504
<212> PRT
<213> Glycine max

<400> 16
Met Ala Ile Ser Asp Glu Pro Glu Ser Val Ala Thr Ala Leu Asn His
1 5 10 15
Ser Ser Leu Arg Arg Arg Pro Ser Ala Thr Ser Thr Ala Gly Leu Phe
20 25 30
Asn Ser Pro Glu Thr Thr Thr Asp Ser Ser Gly Asp Asp Leu Ala Lys
35 40 45

WO 00/32756

Asp Ser Gly Ser Asp Asp Ser Ile Asn Ser Asp Asp Ala A Val Asn
 50 55 60
 Ser Gln Gln Gln Asn Glu Lys Gln Asp Thr Asp Phe Ser Val Leu Lys
 65 70 75 80
 Phe Ala Tyr Arg Pro Ser Val Pro Ala His Arg Lys Val Lys Glu Ser
 85 90 95
 Pro Leu Ser Ser Asp Thr Ile Phe Arg Gln Ser His Ala Gly Leu Phe
 100 105 110
 Asn Leu Cys Ile Val Val Leu Val Ala Val Asn Ser Arg Leu Ile Ile
 115 120 125
 Glu Asn Leu Met Lys Tyr Gly Trp Leu Ile Lys Ser Gly Phe Trp Phe
 130 135 140
 Ser Ser Lys Ser Leu Arg Asp Trp Pro Leu Phe Met Cys Cys Leu Ser
 145 150 155 160
 Leu Val Val Phe Pro Phe Ala Ala Phe Ile Val Glu Lys Leu Ala Gln
 165 170 175
 Arg Lys Cys Ile Pro Glu Pro Val Val Val Val Leu His Ile Ile Ile
 180 185 190
 Thr Ser Thr Ser Leu Phe Tyr Pro Val Leu Val Ile Leu Arg Cys Asp
 195 200 205
 Ser Ala Phe Val Ser Gly Val Thr Leu Met Leu Phe Ser Cys Val Val
 210 215 220
 Trp Leu Lys Leu Val Ser Tyr Ala His Thr Asn Tyr Asp Met Arg Ala
 225 230 235 240
 Leu Thr Lys Leu Val Glu Lys Gly Glu Ala Leu Leu Asp Thr Leu Asn
 245 250 255
 Met Asp Tyr Pro Tyr Asn Val Ser Phe Lys Ser Leu Ala Tyr Phe Leu
 260 265 270
 Val Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Thr Pro Tyr
 275 280 285
 Ile Arg Lys Gly Trp Leu Phe Arg Gln Leu Val Lys Leu Ile Ile Phe
 290 295 300
 Thr Gly Val Met Gly Phe Ile Ile Asp Gln Tyr Ile Asn Pro Ile Val
 305 310 315 320
 Gln Asn Ser Gln His Pro Leu Lys Gly Asn Leu Leu Tyr Ala Thr Glu
 325 330 335
 Arg Val Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys Met
 340 345 350
 Phe Tyr Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu Leu
 355 360 365

Arg Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys Thr
 370 375 380
 Val Glu Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp Met
 385 390 395 400
 Ile Arg His Leu Tyr Phe Pro Cys Leu Arg His Gly Leu Pro Lys Ala
 405 410 415
 Ala Ala Leu Leu Ile Ala Phe Leu Val Ser Ala Leu Phe His Glu Leu
 420 425 430
 Cys Ile Ala Val Pro Cys His Ile Phe Lys Leu Trp Ala Phe Gly Gly
 435 440 445
 Ile Met Phe Gln Val Pro Leu Val Leu Ile Thr Asn Tyr Leu Gln Asn
 450 455 460
 Lys Phe Arg Asn Ser Met Val Gly Asn Met Ile Phe Trp Phe Ile Phe
 465 470 475 480
 Ser Ile Leu Gly Gln Pro Met Cys Val Leu Leu Tyr Tyr His Asp Leu
 485 490 495
 Met Asn Arg Lys Gly Lys Leu Asp
 500

<210> 17
 <211> 470
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (372)

<220>
 <221> unsure
 <222> (424)

<220>
 <221> unsure
 <222> (442)

<220>
 <221> unsure
 <222> (446)

<220>
 <221> unsure
 <222> (469)

<400> 17
 taaacacgct cgctcggtct tcttttccaa tggcgatttc cgatgagcct gaaactgtag 60
 ccaactgctct caaccactct tccctgcgcc gccgtccac cgccgctggc ctcttcaatt 120
 cgcccagac gaccaccgac agttccggtg atgaattggc caaggattcc ggttccgacg 180
 actccatcag cagcgacgcc gccaatcgc aaccgcaaca aaaacaagac actgatttct 240
 ccgtcctcaa attcgcttac cgtccttcgc tccccgctca tcgcaaagtg aaggaaagtc 300
 cgctcagctc ccgacacat tttccgctcag aagtcacgcg gggcctcttc aacctcctgt 360

atagtaagtc cntgttgctg tgaataagcc gactcatcat tgagaatttt aaatgaaata 420
 tggnttgggt tgatcaaac cnggcntttt gggtaaagct caaagtcant 470

<210> 18
 <211> 38
 <212> PRT
 <213> Glycine max

<400> 18
 Asp Phe Ser Val Leu Lys Phe Ala Tyr Arg Pro Ser Val Pro Ala His
 1 5 10 15

Arg Lys Val Lys Glu Ser Pro Leu Ser Ser Asp Thr Ile Phe Val Arg
 20 25 30

Ser His Ala Gly Pro Leu
 35

<210> 19
 <211> 646
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (240)

<220>
 <221> unsure
 <222> (311)

<220>
 <221> unsure
 <222> (337)

<220>
 <221> unsure
 <222> (354)

<220>
 <221> unsure
 <222> (370)

<220>
 <221> unsure
 <222> (383)

<220>
 <221> unsure
 <222> (388)

<220>
 <221> unsure
 <222> (423)

<220>
 <221> unsure
 <222> (431)

<220>

<221> unsure

<222> (435)

<220>

<221> unsure

<222> (463)

<220>

<221> unsure

<222> (486)

<220>

<221> unsure

<222> (503)

<220>

<221> unsure

<222> (540)

<220>

<221> unsure

<222> (547)

<220>

<221> unsure

<222> (616)

<220>

<221> unsure

<222> (633)

<220>

<221> unsure

<222> (639)

<400> 19

```

ctccgacgcc atcttccgac agagccatgc aggtcttctg aatctatgca ttgttgtgct 60
gattgcagtg aacagcaggc tcattattga gaacttaatg aagtatggcc tattaataag 120
agctggggtt tggtttaagt gcaagatcgc tgggagattg gccacttctg atgtgctgcc 180
tcactttacc cathttccca cttgctgctc tcatgaccgg agaattgggt caaaagaaan 240
tcatccgtgg atcatgtgtc tatcctcccc catataatta ttacaaccac tgtccttatc 300
ctatccgggtg ntgtgatcct taaagtgtga accacantat atcctgggtt gtgnttatgt 360
ccattgcaan atacttgggt gancttgncc cttttgctcc atacaattag atataagtat 420
tgnccccc aaa ntatngaaag ggtgctacac agggattcta ccnagaagaa aattaaagcc 480
caactncaac aagtgtgtat cangttggcc caacactggt acaaccaatt taccggcan 540
attatanaaa ggtggtcacc ggaactataa agtgtatttt aagcttatgg ctcaaattggc 600
ataataacca ttggnatca acacatgacg aanttttgnc atgaaa 646

```

<210> 20

<211> 39

<212> PRT

<213> Triticum aestivum

<400> 20

```

Ser Asp Ala Ile Phe Arg Gln Ser His Ala Gly Leu Leu Asn Leu Cys
  1              5              10              15

```

```

Ile Val Val Leu Ile Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu
      20              25              30

```

Met Lys Tyr Gly Leu Leu Ile
35

<210> 21
<211> 1975
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (93)

<400> 21
acgagggcct aggtcgccct cgcactgtg tcagcgcgca agtcggccgc ctccctccgc 60
tttmcgcttt tgcgcgtcmg tgcgtggcgc ggnccaccac catcgcatgt caaaagggaa 120
cccagaccgc caccctcccc gcagcttcct cccctccac ggcgggccgc caccgaaacc 180
caaaaccccc ccccgaaact tccggaacct cccctccagt tccacccatg gccccgcccc 240
gtccgtggcc gctgccacga tcgcgacgac cccctccctc gcctccgcgc cgcctccgc 300
gccgacggtc cagcgagagg cggcgcatgg agcagccgca gcggcacgac gagatgccct 360
gctaccgggc gtccggcgccg cccaccgccc ggtcaaggag agcccgtta gctccgacgc 420
catcttccga cagagccatg caggtcttct gaatctatgc attgttgtgc tgattgcagt 480
gaacagcagg ctcatatcgc agaacttaat gaagtatggc ctattaataa gagctgggtt 540
ttggtttagt gcaagatcgc tgggagattg gccacttctg atgtgctgcc tcactttacc 600
cattttccca ctgtgtgctc tcatgaccga gaagtgggct caaagaaagc tcatccgtga 660
tcatgtgtct attcttctcc atataattat tacaaccact gtccctatct atccggttgt 720
tgtgattctt aagtgtgaat cagcagtatt atctggattt gtgttaatgt tcattgcaag 780
cattacttgg ttgaagcttg tctcttttgc tcatacaaat tatgatataa ggatattgtc 840
ccaaagtatt gaaaagggtg ctacacatgg cagttctatc gatgaggaaa acattaaagg 900
cccaactatc aacagtgttg tgtatttcat gttggcccca acactttgtt accagccaag 960
ttatccccgg acagcattta ttagaaaagg ctgggtcacc cggcagctta taaaatgtgt 1020
agtttttaca ggcttgatgg gcttcataat tgagcaatac attaatccaa ttgtgcagaa 1080
ttcgaagcat ccattgaacg gaaatttctt ggaatgctatt gagagagtct tgaaactctc 1140
agtgccaaca ttatatgtat ggctttgtat gttctattcc ttttccatc tgtggttgaa 1200
tattctagcc gaactcctcc gttttggtga tcgtgaattc tacaaggact ggtggaacgc 1260
caaaacagtt gaagagtact ggagaatgtg gaatatgcct gttcataagt ggatcggtcg 1320
acatatatat tttccatgca taaggaaatgg cttatcaaag ggttggtgcca ttctcctgc 1380
atttctggtt tcagctgtat ttcattgagc atgtattgct gttccgtgcc acattttcaa 1440
attatgggca ttttctggaa tcatgtttca gattcccttg ctattcttga cgaaatatct 1500
tcaagataag ttcaagaata caatggtggg caacatgata ttttggttct tcttcagcat 1560
agttgggcaa ccaatgtgtg ttctcttgta ctaccatgat gtcattgaaca gacaggctca 1620
gacaaatggc tagttctgtt ttagaagtgc actataaac agatcgctcg aagcaaatg 1680
gcccagggca atggaggggc ggctcctta atgtttcgcc atgggctgtt agagcttgct 1740
atgctacgaa tccaagtttg tcagcatgat atgttccaat ccgttccagt tagctcgtg 1800
cgttccaaat gtatgatatg cggcgccggg tgtgtaccga agatacccca gtgatgaagc 1860
cgaagataac acgacctgcc acatgtgtt tgtgtatacg tttcggttca tgtgccagca 1920
gagttacgta cgtgatgccc tggttgatat aaagtgtacg tgccgtatga aaaaa 1975

<210> 22
<211> 508
<212> PRT
<213> Triticum aestivum

<400> 22
Met Ser Lys Gly Asn Pro Asp Pro His Leu Pro Gly Ser Phe Leu Pro
1 5 10 15
Ser His Gly Gly Pro Pro Pro Lys Pro Lys Thr Pro Pro Arg Thr Phe
20 25 30

Arg Asn Leu Pro Ser Ser Ser Thr His Gly Pro Ala Pro Ser Val Ala
 35 40 45
 Ala Ala Thr Ile Ala Thr Thr Pro Pro Ser Ala Ser Ala Ala Pro Leu
 50 55 60
 Pro Pro Thr Val His Gly Glu Ala Ala His Gly Ala Ala Ala Ala Ala
 65 70 75 80
 Arg Arg Asp Ala Leu Leu Pro Gly Val Gly Ala Ala His Arg Arg Val
 85 90 95
 Lys Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe Arg Gln Ser His Ala
 100 105 110
 Gly Leu Leu Asn Leu Cys Ile Val Val Leu Ile Ala Val Asn Ser Arg
 115 120 125
 Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Leu Leu Ile Arg Ala Gly
 130 135 140
 Phe Trp Phe Ser Ala Arg Ser Leu Gly Asp Trp Pro Leu Leu Met Cys
 145 150 155 160
 Cys Leu Thr Leu Pro Ile Phe Pro Leu Ala Ala Leu Met Thr Glu Lys
 165 170 175
 Trp Ala Gln Arg Lys Leu Ile Arg Asp His Val Ser Ile Leu Leu His
 180 185 190
 Ile Ile Ile Thr Thr Thr Val Leu Ile Tyr Pro Val Val Val Ile Leu
 195 200 205
 Lys Cys Glu Ser Ala Val Leu Ser Gly Phe Val Leu Met Phe Ile Ala
 210 215 220
 Ser Ile Thr Trp Leu Lys Leu Val Ser Phe Ala His Thr Asn Tyr Asp
 225 230 235 240
 Ile Arg Ile Leu Ser Gln Ser Ile Glu Lys Gly Ala Thr His Gly Ser
 245 250 255
 Ser Ile Asp Glu Glu Asn Ile Lys Gly Pro Thr Ile Asn Ser Val Val
 260 265 270
 Tyr Phe Met Leu Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg
 275 280 285
 Thr Ala Phe Ile Arg Lys Gly Trp Val Thr Arg Gln Leu Ile Lys Cys
 290 295 300
 Val Val Phe Thr Gly Leu Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn
 305 310 315 320
 Pro Ile Val Gln Asn Ser Lys His Pro Leu Asn Gly Asn Phe Leu Asp
 325 330 335
 Ala Ile Glu Arg Val Leu Lys Leu Ser Val Pro Thr Leu Tyr Val Trp
 340 345 350

Leu Cys Met Phe Tyr Ser Phe Phe His Leu Trp Leu Asn Ile Leu Ala
 355 360 365

Glu Leu Leu Arg Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn
 370 375 380

Ala Lys Thr Val Glu Glu Tyr Trp Arg Met Trp Asn Met Pro Val His
 385 390 395 400

Lys Trp Ile Val Arg His Ile Tyr Phe Pro Cys Ile Arg Asn Gly Leu
 405 410 415

Ser Lys Gly Cys Ala Ile Leu Ile Ala Phe Leu Val Ser Ala Val Phe
 420 425 430

His Glu Leu Cys Ile Ala Val Pro Cys His Ile Phe Lys Leu Trp Ala
 435 440 445

Phe Ser Gly Ile Met Phe Gln Ile Pro Leu Leu Phe Leu Thr Lys Tyr
 450 455 460

Leu Gln Asp Lys Phe Lys Asn Thr Met Val Gly Asn Met Ile Phe Trp
 465 470 475 480

Phe Phe Phe Ser Ile Val Gly Gln Pro Met Cys Val Leu Leu Tyr Tyr
 485 490 495

His Asp Val Met Asn Arg Gln Ala Gln Thr Asn Gly
 500 505

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 23

cttagcttct tccttcaatc

20

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 24

tttctagact cgagtgaaca gttgtttcat gac

33

<210> 25

<211> 497

<212> PRT

<213> Mus musculus

<400> 25

Met Gly Asp Arg Gly Gly Ala Gly Ser Ser Arg Arg Arg Thr Gly Ser
 1 5 10 15

Arg Val Ser Val Gln Gly Gly Ser Gly Pro Lys Val Glu Glu Asp Glu
 20 25 30
 Val Arg Asp Ala Ala Val Ser Pro Asp Leu Gly Ala Gly Gly Asp Ala
 35 40 45
 Pro Ala Pro Ala Pro Ala Pro Ala His Thr Arg Asp Lys Asp Gly Arg
 50 55 60
 Thr Ser Val Gly Asp Gly Tyr Trp Asp Leu Arg Cys His Arg Leu Gln
 65 70 75 80
 Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr Arg Gly Ile
 85 90 95
 Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala Arg Leu Phe
 100 105 110
 Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro Ile Gln Val
 115 120 125
 Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala Pro Cys Val
 130 135 140
 Ile Ile Ala Ser Asn Ile Phe Val Val Ala Ala Phe Gln Ile Glu Lys
 145 150 155 160
 Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Met Gly Leu Leu Leu His
 165 170 175
 Val Val Asn Leu Ala Thr Ile Ile Cys Phe Pro Ala Ala Val Ala Leu
 180 185 190
 Leu Val Glu Ser Ile Thr Pro Val Gly Ser Val Phe Ala Leu Ala Ser
 195 200 205
 Tyr Ser Ile Met Phe Leu Lys Leu Tyr Ser Tyr Arg Asp Val Asn Leu
 210 215 220
 Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser Thr Gly Lys
 225 230 235 240
 Lys Val Ser Gly Ala Ala Ala Gln Gln Ala Val Ser Tyr Pro Asp Asn
 245 250 255
 Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro Thr Leu Cys
 260 265 270
 Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe Leu
 275 280 285
 Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu Gln Val Gly
 290 295 300
 Leu Ile Gln Gln Trp Met Val Pro Thr Ile His Asn Ser Met Lys Pro
 305 310 315 320
 Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu Leu Lys Leu
 325 330 335

Ala	Val	Pro	Asn	His	Leu	Ile	Trp	Leu	Ile	Phe	Phe	Tyr	Trp	Phe	Phe
			340					345					350		
His	Ser	Cys	Leu	Asn	Ala	Val	Ala	Glu	Leu	Leu	Gln	Phe	Gly	Asp	Arg
		355					360					365			
Glu	Phe	Tyr	Arg	Asp	Trp	Trp	Asn	Ala	Glu	Ser	Val	Thr	Tyr	Phe	Trp
	370					375					380				
Gln	Asn	Trp	Asn	Ile	Pro	Val	His	Lys	Trp	Cys	Ile	Arg	His	Phe	Tyr
385					390					395					400
Lys	Pro	Met	Leu	Arg	His	Gly	Ser	Ser	Lys	Trp	Val	Ala	Arg	Thr	Gly
			405						410					415	
Val	Phe	Leu	Thr	Ser	Ala	Phe	Phe	His	Glu	Tyr	Leu	Val	Ser	Val	Pro
			420					425					430		
Leu	Arg	Met	Phe	Arg	Leu	Trp	Ala	Phe	Thr	Ala	Met	Met	Ala	Gln	Val
		435					440					445			
Pro	Leu	Ala	Trp	Ile	Val	Gly	Arg	Phe	Phe	Gln	Gly	Asn	Tyr	Gly	Asn
	450					455					460				
Ala	Ala	Val	Trp	Val	Thr	Leu	Ile	Ile	Gly	Gln	Pro	Val	Ala	Val	Leu
465					470					475					480
Met	Tyr	Val	His	Asp	Tyr	Tyr	Val	Leu	Asn	Tyr	Asp	Ala	Pro	Val	Gly
				485					490					495	

Val

```
<210> 26
<211> 520
<212> PRT
<213> Arabidopsis thaliana
```

<400> 26																
Met	Ala	Ile	Leu	Asp	Ser	Ala	Gly	Val	Thr	Thr	Val	Thr	Glu	Asn	Gly	
1				5					10					15		
Gly	Gly	Glu	Phe	Val	Asp	Leu	Asp	Arg	Leu	Arg	Arg	Arg	Lys	Ser	Arg	
			20					25					30			
Ser	Asp	Ser	Ser	Asn	Gly	Leu	Leu	Leu	Ser	Gly	Ser	Asp	Asn	Asn	Ser	
		35					40					45				
Pro	Ser	Asp	Asp	Val	Gly	Ala	Pro	Ala	Asp	Val	Arg	Asp	Arg	Ile	Asp	
	50					55					60					
Ser	Val	Val	Asn	Asp	Asp	Ala	Gln	Gly	Thr	Ala	Asn	Leu	Ala	Gly	Asp	
65					70					75					80	
Asn	Asn	Gly	Gly	Gly	Asp	Asn	Asn	Gly	Gly	Gly	Arg	Gly	Gly	Gly	Glu	
				85					90					95		
Gly	Arg	Gly	Asn	Ala	Asp	Ala	Thr	Phe	Thr	Tyr	Arg	Pro	Ser	Val	Pro	
			100					105					110			

Ala His Arg Arg Ala Arg Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe
 115 120 125
 Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Val Val Val Leu Ile
 130 135 140
 Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Trp
 145 150 155 160
 Leu Ile Arg Thr Asp Phe Trp Phe Ser Ser Arg Ser Leu Arg Asp Trp
 165 170 175
 Pro Leu Phe Met Cys Cys Ile Ser Leu Ser Ile Phe Pro Leu Ala Ala
 180 185 190
 Phe Thr Val Glu Lys Leu Val Leu Gln Lys Tyr Ile Ser Glu Pro Val
 195 200 205
 Val Ile Phe Leu His Ile Ile Ile Thr Met Thr Glu Val Leu Tyr Pro
 210 215 220
 Val Tyr Val Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Val Thr
 225 230 235 240
 Leu Met Leu Leu Thr Cys Ile Val Trp Leu Lys Leu Val Ser Tyr Ala
 245 250 255
 His Thr Ser Tyr Asp Ile Arg Ser Leu Ala Asn Ala Ala Asp Lys Ala
 260 265 270
 Asn Pro Glu Val Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe
 275 280 285
 Met Val Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Ser Ala
 290 295 300
 Cys Ile Arg Lys Gly Trp Val Ala Arg Gln Phe Ala Lys Leu Val Ile
 305 310 315 320
 Phe Thr Gly Phe Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile
 325 330 335
 Val Arg Asn Ser Lys His Pro Leu Lys Gly Asp Leu Leu Tyr Ala Ile
 340 345 350
 Glu Arg Val Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys
 355 360 365
 Met Phe Tyr Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu
 370 375 380
 Leu Cys Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys
 385 390 395 400
 Ser Val Gly Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp
 405 410 415
 Met Val Arg His Ile Tyr Phe Pro Cys Leu Arg Ser Lys Ile Pro Lys
 420 425 430

Thr Leu Ala Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu
435 440 445

Leu Cys Ile Ala Val Pro Cys Arg Leu Phe Lys Leu Trp Ala Phe Leu
450 455 460

Gly Ile Met Phe Gln Val Pro Leu Val Phe Ile Thr Asn Tyr Leu Gln
465 470 475 480

Glu Arg Phe Gly Ser Thr Val Gly Asn Met Ile Phe Trp Phe Ile Phe
485 490 495

Cys Ile Phe Gly Gln Pro Met Cys Val Leu Leu Tyr Tyr His Asp Leu
500 505 510

Met Asn Arg Lys Gly Ser Met Ser
515 520